Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended) A method of identifying a hairpin nucleic acid ~~probes~~ probe that hybridizes over its entire length to a target nucleic acid molecule, the method comprising:

providing a target nucleic acid sequence that is larger than about 100 nucleotides in length;

predicting a folded structure of the target nucleic acid sequence;

identifying a nucleotide sequence of a hairpin within the folded structure of the target nucleic acid sequence; and

predicting a folded structure for the identified nucleotide sequence of the hairpin, in the absence of other nucleotides of the target nucleic acid sequence, wherein the folded structure of ~~the~~ a hairpin that has a predicted E value of at most about - 3 kcal/mol is a probe that hybridizes over its entire length to the target nucleic acid molecule.

2. (Original) The method according to claim 1 wherein the nucleotide sequence of the hairpin is between about 12 and about 60 nucleotides in length.

3. (Original) The method according to claim 1 wherein the folded structure of the hairpin has a predicted E value of between about - 4 kcal/mol and about - 12 kcal/mol.

4. (Original) The method according to claim 1 further comprising:

predicting a folded structure of a duplex formed between the hairpin and its complement.

5. (Original) The method according to claim 4 further comprising:

determining whether duplex formation is energetically favorable.

6. (Original) The method according to claim 1 further comprising:

performing a database search for nucleotide sequences that are similar to the identified nucleotide sequence of the hairpin.

7. (Original) The method according to claim 6 further comprising:

determining, from the results of the performed database search, whether a clear demarcation exists between scores for target nucleic acid sequences and scores for non-target nucleic acid sequences.

8. (Currently Amended) ~~The~~ A method of preparing a molecular beacon comprising:

providing a hairpin nucleic acid probe identified according to the method of claim 1; and

tethering a fluorescent label and a quenching agent to the opposed termini of the provided hairpin nucleic acid probe to form a molecular beacon, wherein the molecular beacon is substantially non-fluorescent in the absence of a nucleic acid complementary to the hairpin nucleic acid probe.

9. (Original) The method according to claim 8, wherein said providing comprises:

synthesizing a nucleic acid molecule corresponding to the nucleotide sequence of the hairpin probe.

10. (Original) The method according to claim 8, wherein the fluorescent label is tethered to the 5' terminus and the quenching agent is tethered to the 3' terminus.

11. (Original) The method according to claim 8, wherein the fluorescent label is tethered to the 3' terminus and the quenching agent is tethered to the 5' terminus.

12. (Original) The method according to claim 8, wherein the quenching agent is a solid surface.

13. (Original) The method according to claim 8, wherein the quenching agent is a micro- or nano-particle.

14. (Original) The method according to claim 8, wherein the fluorescent label is a fluorescent dye, semiconductor quantum dot, lanthanide atom-containing complex, or fluorescent protein.

15. (Original) The method according to claim 8, wherein the quenching agent is a metal or 4-([4-(Dimethylamino)phenyl]azo)benzoic acid.

16. (Original) The method according to claim 15, wherein the metal is gold, silver, platinum, copper, cobalt, iron, or iron-platinum.

17. (Original) A method of preparing a hairpin nucleic acid molecule comprising: synthesizing a hairpin nucleic acid molecule identified according to the method of claim 1.

18-30. (Canceled)

31. (New) A method of identifying a hairpin nucleic acid probe that hybridizes over its entire length to a target nucleic acid molecule, the method comprising:

providing a target nucleic acid sequence that is larger than about 100 nucleotides in length;

predicting a folded structure of the target nucleic acid sequence;

identifying a nucleotide sequence of a hairpin within the folded structure of the target nucleic acid sequence, the hairpin being between about 12 and about 60 nucleotides in length; and

determining whether (i) self-folding of the identified hairpin and (ii) hairpin binding over its entire length to the target nucleic acid molecule will be energetically favorable.